FIGURE 1B

```
1201  CATCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC CTCCAAACAT CTACTACACA TCGATTTCTG TGTTGGAGTG GCCCATATTG CATACGATAC
      GTAGGACACA TATAGCACGT CCTACCCGGG GGGGTCTCGG GAGGTTTGTA GATGATGTGT AGCTAAAGAC ACAACCTCAC CGGGTATAAC GTATGCTATG
 320  HisProValT yrIleValGl nAspGlyPro ProGlnSerP roProAsnIl eTyrTyrThr SerIleSerV alLeuGluTr pProIleLeu HisThrIleGln

1301  AACTGTTTTT CATGCGATCC AAGTGCTCCC GTGTCACTAC ATTCTTATTT CCTGTGCAAG TTATTACGAC ATCGACTTGC CGGATGACTT CATTTAGCTT
      TTGACAAAAA GTACGCTAGG TTCACGAGGG CACAGTGATG TAAGAATAAA GGACACGTTC AATAATGCTG TAGCTGAACG GCCTACTGAA GTAAATCGAA
 354  LeuPhePh eMetArgSer LysCysSerA rgValThrTh rPheLeuPhe ProValGlnV alIleThrTh rSerThrCys ArgMetThrS erPheSerPhe

1401  TACCACCCTG AACCCATCCA TGCAGGCCTG CAGAGCACAG ATGGGGGAAT TCCGAATCAG ATGGTGTTTC TGGGGGGACA GGATCCTGGG TACGGCTCTG
      ATGGTGGGAC TTGGGTAGGT ACGTCCGGAC GTCTCGTGTC TACCCCCTTA AGGCTTAGTC TACCACAAAG ACCCCCCTGT CCTAGGACCC ATGCCGAGAC
 387  ThrThrLeu AsnProSerM etGlnAlaCy sArgAlaGln MetGlyGluP heArgIleAr gTrpCysPhe rgIleLeuGl yThrAlaLeu

 501  TTTGTGCTTG TGCTTATTCT TCTTCTTGGG AGGCTGAATA TGCATCAGAC GACACTGCTC CGGCAACGGG CCAGTGTGGA GGCGGAAGCC GGCCAGCATG
      AAACACGAAC ACGAATAAGA AGAAGAACCC TCCGACTTAT ACGTAGTCTG CTGTGACGAG GCCGTTGCCC GGTCACACCT CCGCCTTCGG CCGGTCGTAC
 420  PheValLeuV alLeuIleLe uLeuLeuGly ArgLeuAsnM etHisGlnTh rThrLeuLeu laSerValGl uAlaGluAla GlyGlnHisGly

1601  GTCCCCTGTG ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG TTATCATGGG AACCAGGCAG ATCAATCATC
      CAGGGGACAC TATCCTAACT TTCTCGATGA CTCTTATCCC CCGAAGAGTT ACTCTCTCGC AATAGTACCC TTGGTCCGTC TAGTTAGTAG
 454  ProLeu     (SEQ ID NO: 2)

1701  CCTGGCAGGT CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG
      GGACCGTCCA GTCCGTCCTT CAATGAATCG AAGAGGAAGT GGAAGAAGGG TGTCTTAAAT AATATCCGAA CAAGGTTCAA CATCACACAC TAGTCTAAGC

1801  TGCTGCCTGT CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGGAATTGGA TATCAAGCTT ATCGATACCG TCGACCT  (SEQ ID NO: 1)
      ACGACGGACA GTCGAGACAC GATGGACCGT CAAGGGGAGT ACCTTAACCT ATAGTTCGAA TAGCTATGGC AGCTGGA
```

FIGURE 2B

```
1101 GGAGGCTGAG CCTGGGGAGC TAGGGATAGC TCTGCGGGGT GGGGGGCTG CAGATCCCCC CTTCTGCCC CACTATGAGA AGGTGAGTGG TGACTGTGGG
     CCTCCGACTC GGACCCCTCG ATCCCTATCG AGAGCCCCA CCGCCCCGAC GTCTAGGGGG GAAGACGGGG GTGATACTCT TCCACTCACC ACTGATACCC
 287   GluAlaGlu ProGlyGluL euGlyIleAl aLeuArgGly GlyGlyAlaA laAspProPr HisTyrGluL ysValSerGl yAspTyrGly

1201 CATCCCTGTGT ATATCGTGCA GGATGGGCCC CCCCAGAGCC GTATGAGGGC CTACTACAAG CTACTACAAG GTATGAGGGC TGGCTATCCT GAATCCAGCC
     GTAGGACACA TATAGCACGT CCTACCCGGG GGGGTCTCGG GATGATGTTA GATGATGTTC CATACTCCCG AGGAGAGTGC ACCGATAGGA CTTAGGTCGG
 320  HisProValT yrIleValGl uAspGlyPro ProGlnSerP roProAsnIl eTyrTyrLys ValTyrGluL       (SEQ ID NO: 4)

1301 CTTCTTGGGG TGCTCCTCCA GTTTAATTCC TGGTTTGAGG GACACCTCTA ACATCTCGGC CCCCTCTGCC CTTCACTCCT CCCGGCTGCT
     GAAGAACCCC ACGAGGAGGT CAAATTAAGG ACCAAACTCC CTGTGGAGAT TGTAGAGCCG GGGGGTCGG GAAGTGAGGA GGGCCGACGA

1401 GTCCTCGTCT CCACTTTTAG GATTCCTTAG GATTCCCACT CCCCCACTTC CTGCCCTCCC GTTTGGCCAT GGTCGCCCCC CTCTCGTCTCA GTGTCCCTGG
     CAGGAGCAGA GGTGAAATC CTAAGGAATC CTAAGGGTGA GGGGGTGAAG GACGGGAGGG CAAAACCGTA CCCACGGGGG GAGACAGAGT CACAGGGACCC

1501 ATCCTTTTTC CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATG ACCCAGGCCAT CCTTGTCCCC CTCACCCACC CAGAGCTAGG GGCGGGAACA
     TAGGAAAAAG GAACCCCTCC CCGTGTCCGA GTCGGAGGAG AGACTGGTAC TGGGTCCGTA GGAACAGGGG GTCTCGGATCC CCGCCCTTGT

1601 GCCCACCTTT TGGTTGGCAC CGCCTTCTTT CTGTTTTTCT CTTCTATTCT TCCTTCTTTT CCGTCTCTAG GTCTGTTCTT
     CGGGTGGAAA ACCAACCGTG GCGGAAGAAA GACGAAAGA TCTTATTCT TCTTATTCT AGGGAGAGAA GGCAGAGATC CAGACAAGAA

1701 CTTCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCTC ATCCTGTGCC TCTCCCATCT TCTCCCATCT AGAGGGTAGA CATTCTCCC
     GAAGGGATCG TAGGAGGAGG GGTGTAGAGG AAAGTGGGAG AGACGTAGGC TAGGACACGG AGAGGGTAGA CCCTAGTTTC GTAAAGAGGG

1801 CTTAGCTTTC AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCTCAG TCTGCCAAAA ATGGGGGCCT TATGGGAAG GCTCTGACAC TCCACCCCAG
     GAATCGAAAG TCGGGGGAA GACTGGAGAG TATGGTTGGT GAGGGGAGTC GAGGGGTTT TACCCCGGA ATACCCTTC CGAGACTGTG AGGTGGGGTC

1901 CTCAGGCCAT GGGCACCAGG GCTCCATTCT CTGGCCTGGC CCAGGCCTCT ACATACTTAC TCCAGCCATT TGGGGTGGTT AGCTACCATG
     GAGTCCGGTA CCCGTCGTCC CGAGGTAAGA GACCGGACCG GGTCCGGAGA TGTATGAATG AGGTCGGTAA ACCCCACCAA CCCAGTACTG TCGATGGTAC

2001 AGAAGAAGTG TCCCGTTTTC TCCACTGGCC AATAGCAAGA TATGGACATG TGGGAAGTAG GTCTCATGCT GAATGGGCCA CTTGGGACCG
     TCTTCTTCAC AGGGCAAAAC AGGTCACCGG TTATCGTTCT ATACTTGGCC AGCCCTGTAC CAGACTACGA CTTACCCGGT GAACCCTGGC

2101 GAAGTGACTT GCTCCAGACA AGAGGTGACC AGCCCCGGAC AGAAATGGCC AGAAGCAGT CAGAAGCAGG CTGGAAGTGC CTTCATCCAG
     CTTCACTGAA CGAGGTCTGT TCTCCACTGG TCGGGGCCTG TCTTTACGG GTCTTCGTCA CGTCGTCCTT GACCTTCAGG GAAGTAGGTC

2201 GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACTCCAA TGGGGGATC CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT
     CTGTCCTTCA TCGTGAAGAC TTTGTCCTTC ACCAGACCGA CCTTGAGGTT CACCGAATCA TCCTCCACCC GACCCCTAG TCCAACTACC AAGAATAAGA

2301 GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA CCTGGAACTT ACTGACTGTA GGTGGACCGA        (SEQ ID NO: 3)
     CACCTCTTCT TCCCGCCCTT CTTGAAGGAA AGTCCTCCTT GGACCTTGAA TGACTGACAT TCTCCAATCT CCACCTGGCT
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TOTAL P.04

FIGURE 3A

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AL-2b.L      1  GNTCTAGAANTAGTGGATCCCCCCGGGCTGCAGGAATTCCGACGGCCCT

AL-2b.L     51  GGAAGGGCTCTGGTGGGGCTGAGCGCTCTGCCGCGGGGCGCGGGGAGAG

AL-2b.L    101  CAGGAAGCAGGTCCGCGTGGGCGCTGGGGGCATCAGCTACCGGGGTGGTC

AL-2b.L    151  CGGGCTGAAGAGCCAGGCAGCCAAGGCAGCCACCCCGGGGGGTGGGCGAC

AL-2b.L    201  TTTGGGGGAGTTGGTGCCCCGCCCCCCAGGCCTTGGCGGGGTCATGGCGC

AL-2b.L    251  CCCCCCATTCTGGGCCGGGGGGCGTGCGAGTCGGGGCCCTGCTGCTGCTG

AL-2b.L    301  GGGGTTTTGGGGCTGGTGTCTGGGCTCAGCCTGGAGCCTGTCTACTGGAA

AL-2b.L    351  CTCGGCGAATAAGAGGTTCCAGGCAGAGGGTGGTTATGTGCTGTACCCTC

AL-2b.L    401  AGATCGGGGACCGGGTAGACGTGCTCTGCCCCCGGGGCCGGGCTCCTGGC

AL-2b.L    451  CCTCACTCCTCTCCTAATTATGAGTTCTACAAGCTGTACCTGGTAGGGGG

AL-2b.L    501  TGCTCAGG[GGCGG][CGGTGTGAGGCAGCCCCTGCCCCAAACCTCCTTCTCA
H10006       1  ........[GCCGA][CGGTGTGAGGCAGCCCCTGCCCCAAACCTCCTTCTCA

AL-2b.L    551  [CTTGTGATCGCCCAGACCTGGATCTCCGGCTTCACCATCAAGTTCCAGGAG
H10006      43  [CTTGTGATCGCCCAGACCTGGATCTCCGGCTTCACCATCAAGTTCCAGGAG

AL-2b.L    601  [TATAGCCCTAATGTGTGGGGCGACGAGTTCCGGCTCGCACCACGATTACTA
H10006      93  [TATAGCCCTAATGTGTGGGGCCACGAGTTCCGGGTCGCACCACGATTACTA

AL-2b.L    652  [CATCATTGCCACATCGGATGGGACCCGGGGAGG[G][C]T[GGAGAGCCTGCAGG]
H10006     145  [CATCATTCCCACATCGGATGGGACCCGGGAGG[G][C]T[GGAGAGCCTGCAGG]

AL-2b.L    702  [GA][G][GTGTGTGCCTAACCAGAGGCATGAAGGTGCTTCTCCGAGT][GGACAA]
H10006     193  [GA][A][GTGTGTGCCTAACCAGAGGCATGAAGGTGCTTCTCGGAGT][N][GGACAA]

AL-2b.L    752  [AGT][C][CCCGAGGAGGGGGCTGTCCCCCGAAAAACCTGTGTCTGAAATGCCCAT]
H10006     243  [AGT][.][CCCGAGGAGGGGGCTGTCCCCCGAAAACC][T]GTGTCTGAAATGCCCAT]

AL-2b.L    802  [GGAAAGAGACCGAGGGGCAGCCCACAGCCT][.][GGAGCCT][.][GGGAAGGAGAA]
H10006     292  [GGAAAGAGACCGAGGGGCAGCCCACAGCCT][GGAGCCT][GGGAAGGAGAA]

AL-2b.L    849  [CCTGGCCAGGTGACCCCACCAGCAAT][G][C]AACCT[C][CCGGGGT]...CC[TGAAGG]
H10006     332  [CCTGGCCAGGTGACCCCACCAGCAAT][N]CAACCT[T][CCGGGCT][TGCT][TGAAGG]

AL-2b.L    897  C[CCCCT]..G[CCC]C[CT][CCCAGCA].[TGC][T][GCAGT]..[GGCT][GGGGCAGCAGG]
H10006     352  G[CCCCT][TGA][CCC]T[TT][CCCAGCA][T][TGC][N][TGCA][NT][G][GTTN][GGGGCAGCANG]

AL-2b.L    942  [GGGG][C].....[TGGC]GCTGCTCTTGCTGGGCGTGGCAGGGCCTGGGGGTGCC
H10006     441  [GGGG][N][GTTT][TGGC]

                                (SEQ ID NO: 5)

AL-2b.L    998  ATGTGTTGGCGGAGACGGGCGGGGCAAGCCTTCGGAGAGTCGCCACCCTGG

AL-2b.L   1048  TCCTGGCTCCTCGGGGAGGGGAGGGTCTCTGGGCCTGGGGGGTGGAGGTG

AL-2b.L   1098  GGATGGGACCTCGGCAGCTGAGCCTGGGGAGGTAGGGATAGGTCTGCGG

AL-2b.L   1148  GGTGGGCGGGGCTGCAGAGCCCCCCTTCTGGCGGCACTATGAGAAGGTGAG
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AL-2b.L  1189  TGGTGACTAT⬤CATCCTGTGTATATCGTGCAGGATGGG⬤CCCCCAGA
AL-2b.L  1233  GCCCTCCAAACATCTACTACACATCGATTTCTGTGTTGGAGTGGCCCATA
AL-2b.L  1283  TTGCATACGATACAACTGTTCTTCATGCGATCCAAGTGCTCCCGTGTCAC
AL-2b.L  1338  TACATTCTTATTTCCTGTGCAAGTTATTACGACATCGACTTGCCGGATGA
AL-2b.L  1388  CTTCATTTAGCTTTACCACCCTGAACCCATCCATGCAGGCCTGCAGAGCA
AL-2b.L  1438  CAGATGGGGGAATTCCGAATCAGATGGTGTTTCTGGGGGGACAGGATCCT
AL-2b.L  1488  GGGTACGGCTCTGTTTGTGCTTGTGCTTATTCTTCTTCTTGGGAGCCTGA
AL-2b.L  1538  ATATGCATCAGACGACACTGCTCCGGCAACGGGCCAGTGTGGAGGCGGAA
AL-2b.L  1588  GCCGGCCAGCATGGTCCCCTGTGATAGGATTGAAAGAGCTACTGAGAATA
AL-2b.L  1638  GGGGGCTTCTCAATGAGAGAGCGCAGGCTGCTGTTATCATGGGAACCAGG
AL-2b.L  1688  CAGATCAATCATCCCTGGCAGGTCAGGCAGGAAGTTACTTAGCTTCTCCT
AL-2b.L  1738  TCACCTTCTTCCCACAGAATTTATTATAGGCTTGTTCCAAGTTGTAGTGT
AL-2b.L  1788  GTGATCAGATTCGTGCTGCCTGTCAGCTCTGTGCTACCTGGCAGTTCCCC
AL-2b.L  1838  TCATGGAATTCGATATCAAGCTTATCGATACCGTCGACCT  (SEQ ID NO: 1)
```

FIGURE 3B

```
lerk2     2   MA-RPGQRWLQKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKG
huHTKL    1   NAVRRQSVWKYCWQVLHV---LCRTAISKGIVLEPIYWNSSVSKFLPGQQ
AL2.sht   1   MG-PPHSGPGGVRVGALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG
AL2.long  1   MG-PPHSGPGGVRVGALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEG3

lerk2     52  LVIYPKIGDKLDIICPRA---EAGR--PYEYYKLYLVRPEQAAACSTVLD
huHTKL    48  LVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQADRCTIKKE
AL2.sht   49  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA
AL2.long  49  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA

lerk2     95  PNYLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKHHDYYITSTGNGSLEG
huHTKL    96  NTPLLNCAKPQQDIKFTIKFQEFSPHLWGLEFQKNKDYYIISTSNGSLEG
AL2.sht   96  PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
AL2.long  96  PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

lerk2     145 LENREGGVCRTRTMKIIMKVCQDPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL    145 LDNQEGGVCQTRAMKILMKVGQDASS------AGSTRNKCPTRPELEAG
AL2.sht   146 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
AL2.long  146 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE

lerk2     195 APGSRQSLGDSDGKHETVNCEEKSGPGASGGSSGDPQGFFNGKVALFAAV
huHTKL    159 TNG-RSSTTSPFVKPNPGSSTDDNSAGHSG-----NNILGSEVALFAGI
AL2.sht   198 -PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL---ALLLLGVA
AL2.long  198 -PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL---ALLLLGVA

lerk2     245 GAGQVIFLLIIFLTVLLLKLRKFHRKHTQ-QRAAALSLSTLASPKGGSQ
huHTKL    233 ASGCIIFIVIITLVLLKYRRHRKHSP-GHTTTLSLSTLAITPKRSGN
AL2.sht   244 GAGGA-----MCWRRRRAKPSESRHPGPGSFGRGGSLGLGG----GGGMG
AL2.long  244 GAGGA-----MCWRRRRAKPSESRHPGPGSFGRGGSLGLGG----GGGMG

lerk2     294 TAGTEPSDIIIPLR---TTENNYCPHYEKVSGCYGHPVYIVQEMPPQSPA
huHTKL    282 NNGSEPSDIIIPLR---TACSVFCPHYEKVSGCYGHPVYIVQEMPPQSPA
AL2.sht   285 PREAEPGELGIALRGGGAADPPFCPHYEKVSGCYGHPVYIVQDGPPQSPP
AL2.long  285 PREAEPGELGIALRGGGAADPPFCPHYEKVSGCYGHPVYIVQDGPPGGPP

lerk2     341 NIYY...............................................
huHTKL    328 NIYY...............................................
AL2.sht   335 NIYY...............................................
AL2.long  335 NIYYTSISVLEWPILHTIQLFFWRSKCSRVTTFLFPVQVITTSTCRMTSF

lerk2     343 ..................................KV...............  (SEQ ID NO: 9)
huHTKL    332 ..................................KV...............  (SEQ ID NO: 10)
AL2.sht   334 ..................................KV...............  (SEQ ID NO: 4)
AL2.long  385 SFTTLNPSMQACRAQMGEFRIRWCPWGDRILQTALFVLVLILLLGRLNMH

AL2.long  435 QTTLLRQRASVEAEAGQHGPL  (SEQ ID NO: 2)
```

FIGURE 4

```
LERK2.1     1  MA-RPGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKG
huHTKL      1  MAVRRDSVWKYCWGVLMV---LCRTAISKSIVLEPIYWNSSNSKFLPGQG
ALII.long   1  MGPPHSGP-GGVRVGALLL--LGVLGLVSGLSLEPVYWNSANKRFQAEGG

LERK2.1    50  LVIYPKIGDKLDIICPRA---EAGR--PYEYYKLYLVRPEQAAACSTVLD
huHTKL     48  LVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQADRCTIKKE
ALII.long  48  YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA

LERK2.1    95  PNVLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITSTSNGSLEG
huHTKL     95  NTPLLNCAKPDQDIKFTIKFQEFSPNWGLEFQKNKDYYIISTSNGSLEG
ALII.long  98  PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

LERK2.1   145  LENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL    145  LDNQEGGVCQTRAMKILMKVGQDASS------AGSTRNKDPTRRPELEAG
ALII.long 148  LESLQGGVCLTRGMKVLLRVGQSPR-------GGAVPRKPVSEMPME-R

LERK2.1   195  APGSRGSLGDSDGKHETVNQEEKSGPGASGGSSGDPDGFFNSKVALFAAV
huHTKL    189  TNG-RSSTTSPFVKPNPGSSTDGNSAGHSG-----NNILGSEVALFAGI
ALII.long 189  DRGAAHSLEPGKENLPGDPTSNATSRGAEG-------PLPPPSMPAVAGA

LERK2.1   245  GAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQRAAALSL---STLASPKGG
huHTKL    232  ASGCIIFIVIIITLVVLLLKYRRRHRKHSPQHTTTLSL---STLATPKRS
ALII.long 232  AGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGG

LERK2.1   292  S-GTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQ
huHTKL    279  G-NNNGSEPSDIIIPLR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQ
ALII.long 282  GMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQ

LERK2.1   338  SPANIYY...........................................
huHTKL    325  SPANIYY...........................................
ALII.long 332  SPPNIYYTSISVLEWPILHTIQLFFMRSKCSRVTTFLFPVQVITTSTCRM

LERK2.1   345  ...............................KV................. (SEQ ID NO:9)
huHTKL    332  ...............................KV................. (SEQ ID NO:10)
ALII.long 382  TSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALFVLVLILLLGRL

ALII.long 432  NMHQTTLLRQRASVEAEAGQHGPL (SEQ ID NO:2)
```

FIGURE 5